

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Goeddel, David V.
Rothe, Mike

(ii) TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors

10 (iii) NUMBER OF SEQUENCES: 66

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: patin (Genentech)

25 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/250858
(B) FILING DATE: 27-MAY-1994

35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/331394
(B) FILING DATE: 28-OCT-1994

40 (viii) ATTORNEY/AGENT INFORMATION:

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5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2088 bases
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 CCCAGCCCGG TTCTCTGCCC CAAGGACGCT ACCGCCCAAT GCGAGCAGAA 50
GGCGGCGCAC AGATACAGAA AGTGAGGCTC AGACATATTG AAGACCGTGT 100
20 GACATAGGGT AGCCAAATGA CAGTGTGAGA AAGTGACATT TACTCAAGGC 150
CACCCAGATA TCCTGGAGGA CCCAGAACCC TGGAGATTCC CATCAGAAAG 200
ACCTTCTGGC CACCTGAAAC CCCAAGATGG CCTCCAGCTC AGCCCCTGAT 250
30 GAAAACGAGT TTCAATTTGG TTGCCCCCCT GCTCCCTGCC AGGACCCATC 300
GGAGCCCAGA GTTCTCTGCT GCACAGCCTG TCTCTCTGAG AACCTGAGAG 350
35 ATGATGAGGA TCGGATCTGT CCTAAATGCA GAGCAGACAA CCTCCATCCT 400
GTGAGCCCAG GAAGCCCTCT GACTCAGGAG AAGGTTCACT CTGATGTAGC 450
40 TGAGGCTGAA ATCATGTGCC CCTTTGCAGG TGTTGGCTGT TCCTTCAAGG 500

GGAGCCCACA ATCCATGCAG GAGCATGAGG CTACCTCCCA GTCCTCCCAC 550

CTGTACCTGC TGCTGGCGGT CTTAAAGGAG TGGAAATCCT CACCAGGCTC 600

CAACCTAGGG TCTGCACCCA TGGCACTGGA GCGGAACCTG TCAGAGCTGC 650

AGCTTCAGGC AGCTGTGGAA GCGACAGGGG ACCTGGAGGT AGACTGCTAC 700

CGGGCACCTT GCTGTGAGAG CCAGGAAGAA CTGGCCCTGC AGCACTTGGT 750

GAAGGAGAAG CTGCTGGCTC AGCTGGAGGA GAAGCTGCGT GTGTTTGCAA 800

ACATTGTTGC TGTCCTCAAC AAGGAAGTGG AGGCTTCCCA CCTGGCACTG 850

GCCGCCTCCA TCCACCAGAG CCAGTTGGAC CGAGAGCACC TCCTGAGCTT 900

GGAGCAGAGG GTGGTGAAT TACAGCAAAC CCTGGCTCAA AAAGACCAGG 950

TCCTGGGCAA GCTTGAGCAC AGTCTGCGAC TCATGGAGGA GGCATCCTTT 1000

GATGGTACTT TCCTGTGGAA GATCACCAAT GTCACCAAGC GGTGCCACGA 1050

GTCAGTGTGT GGCCGGACTG TCAGCCTCTT CTCTCCAGCT TTCTACACTG 1100

CCAAGTATGG TTACAAGTTG TGCCTGCGCT TGTACCTGAA CGGGGATGGC 1150

TCAGGCAAGA AGACCCACCT GTCCCTCTTC ATCGTGATCA TGAGAGGAGA 1200

ATACGATGCT CTCCTGCCCT GGCCTTTCAG GAACAAGGTC ACCTTTATGC 1250

TACTTGACCA GAACAACCGA GAGCATGCTA TTGATGCCTT CCGGCCTGAC 1300

CTGAGCTCAG CCTCCTTCCA GCGGCCACAG AGTGAGACCA ACGTGGCCAG 1350

CGGCTGCCCCG CTCTTCTTCC CCCTCAGCAA GCTGCAGTCA CCCAAGCACG 1400

CCTACGTCAA AGATGACACA ATGTTCTCTCA AATGCATTGT GGACACTAGT 1450

GCTTAGGGAT GGGGGGAGGG GGTGTCTCCT GACAGAACCA GCTTAGACTG 1500

GGGGACTTAG CTAGACAGCC AGGCCCTGCC TGCCCTTGGA GCCCACAGCC 1550

CACGACAAGG AGGAGCCAAG GCTGGCATGA CTCAGCGCC ACAGCATGCT 1600

GGTTATGGCT GATGTGAGGC TGGAGAAACG TGTGCGTACA GAGACAGAGT 1650

GGAGGAGAAG ACAGAAGTGC TCTTTTCACA CAGACTACAC GACACCAGGA 1700

GGCCAGCATG CCAGCAGCTT CTGAATGTTG AGACCAGCCT AGATCAGGAT 1750

GAAAAGAGCC AGGCCTGAGG CTTGGACATT GAGCCAAGGC TATGGGGCCT 1800

AAGTGGAGGG GCACTCCTAC CAGGACATTC TCTCGAGGTC AGGGCATAAC 1850

TGGAAAAATG CCCCCATCTC TCTGTTTCTC CTCAAACTA GAACCACAGG 1900

GCAGAAGGGT CAGACATTAA TGTGAATTTA ACCTGCCCTG GACTGAGTTC 1950

CTATGTTAAC AGACACGCAA ACAGGTAAAC CCAGAACTG CCCTGGGAAA 2000

TGCTTTCTGG CTGCATCTGG AGATCTTTGA TGTTTTTACC GACAAAACAA 2050

ATAACAAAAG CCTTGAATTG CAAAAAAAAA AAAAAAAAAA 2088

5

(2) INFORMATION FOR SEQ ID NO:2:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Ser Ser Ala Pro Asp Glu Asn Glu Phe Gln Phe Gly
1 5 10 15

20 Cys Pro Pro Ala Pro Cys Gln Asp Pro Ser Glu Pro Arg Val Leu
20 25 30

Cys Cys Thr Ala Cys Leu Ser Glu Asn Leu Arg Asp Asp Glu Asp
35 40 45

25 Arg Ile Cys Pro Lys Cys Arg Ala Asp Asn Leu His Pro Val Ser
50 55 60

30 Pro Gly Ser Pro Leu Thr Gln Glu Lys Val His Ser Asp Val Ala
65 70 75

Glu Ala Glu Ile Met Cys Pro Phe Ala Gly Val Gly Cys Ser Phe
80 85 90

35 Lys Gly Ser Pro Gln Ser Met Gln Glu His Glu Ala Thr Ser Gln
95 100 105

Ser Ser His Leu Tyr Leu Leu Leu Ala Val Leu Lys Glu Trp Lys
110 115 120

40 Ser Ser Pro Gly Ser Asn Leu Gly Ser Ala Pro Met Ala Leu Glu
125 130 135

Arg Asn Leu Ser Glu Leu Gln Leu Gln Ala Ala Val Glu Ala Thr

	140	145	150
	Gly Asp Leu Glu Val Asp Cys Tyr Arg Ala Pro Cys Cys Glu Ser		
	155	160	165
5	Gln Glu Glu Leu Ala Leu Gln His Leu Val Lys Glu Lys Leu Leu		
	170	175	180
	Ala Gln Leu Glu Glu Lys Leu Arg Val Phe Ala Asn Ile Val Ala		
10	185	190	195
	Val Leu Asn Lys Glu Val Glu Ala Ser His Leu Ala Leu Ala Ala		
	200	205	210
15	Ser Ile His Gln Ser Gln Leu Asp Arg Glu His Leu Leu Ser Leu		
	215	220	225
	Glu Gln Arg Val Val Glu Leu Gln Gln Thr Leu Ala Gln Lys Asp		
20	230	235	240
	Gln Val Leu Gly Lys Leu Glu His Ser Leu Arg Leu Met Glu Glu		
	245	250	255
	Ala Ser Phe Asp Gly Thr Phe Leu Trp Lys Ile Thr Asn Val Thr		
25	260	265	270
	Lys Arg Cys His Glu Ser Val Cys Gly Arg Thr Val Ser Leu Phe		
	275	280	285
30	Ser Pro Ala Phe Tyr Thr Ala Lys Tyr Gly Tyr Lys Leu Cys Leu		
	290	295	300
	Arg Leu Tyr Leu Asn Gly Asp Gly Ser Gly Lys Lys Thr His Leu		
35	305	310	315
	Ser Leu Phe Ile Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu		
	320	325	330
	Pro Trp Pro Phe Arg Asn Lys Val Thr Phe Met Leu Leu Asp Gln		
40	335	340	345
	Asn Asn Arg Glu His Ala Ile Asp Ala Phe Arg Pro Asp Leu Ser		
	350	355	360

Ser Ala Ser Phe Gln Arg Pro Gln Ser Glu Thr Asn Val Ala Ser
 365 370 375

Gly Cys Pro Leu Phe Phe Pro Leu Ser Lys Leu Gln Ser Pro Lys
 380 385 390

His Ala Tyr Val Lys Asp Asp Thr Met Phe Leu Lys Cys Ile Val
 395 400 405

Asp Thr Ser Ala
 409

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2121 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGCGAAGAC CGTTGGGGCT TTGTGGTGTG TGGGGGTTGT AACTCACATG 50

GCTGCAGCCA GTGTGACTTC CCCTGGCTCC CTAGAACTGC TACAGCCTGG 100

CTTCTCCAAG ACCCTCCTGG GGACCAGGTT AGAAGCCAAG TACCTCTGTT 150

CAGCCTGCAA AAACATCCTG CGGAGGCCTT TCCAGGCCCA GTGTGGGCAC 200

CGCTACTGCT CCTTCTGCCT GACCAGCATC CTCAGCTCTG GGCCCCAGAA 250

CTGTGCTGCC TGTGTCTATG AAGGCCTGTA TGAAGAAGGC ATTTCTATTT 300

TAGAGAGTAG TTCGGCCTTT CCAGATAACG CTGCCCCGAG AGAGGTGGAG 350

AGCCTGCCAG CTGTCTGTCC CAATGATGGA TGCACTTGGA AGGGGACCTT 400

5 GAAAGAATAC GAGAGCTGCC ACGAAGGACT TTGCCCATTC CTGCTGACGG 450

AGTGTCTGC ATGTAAAGGC CTGGTCCGCC TCAGCGAGAA GGAGCACCAC 500

10 ACTGAGCAGG AATGCCCCAA AAGGAGCCTG AGCTGCCAGC ACTGCAGAGC 550

ACCCTGTAGC CACGTGGACC TGGAGGTACA CTATGAGGTC TGCCCCAAGT 600

15 TTCCCTTAAC CTGTGATGGC TGTGGCAAGA AGAAGATCCC TCGGGAGACG 650

TTTCAGGACC ATGTTAGAGC ATGCAGCAAA TGCCGGGTTC TCTGCAGATT 700

20 CCACACCGTT GGCTGTTCAG AGATGGTGGG GACTGAGAAC CTGCAGGATC 750

ATGAGCTGCA GCGGCTACGG GAACACCTAG CCCTACTGCT GAGCTCATTC 800

25 TTGGAGGCCC AAGCCTCTCC AGGAACCTTG AACCAGGTGG GGCCAGAGCT 850

30 ACTCCAGCGG TGCCAGATTT TGGAGCAGAA GATAGCAACC TTTGAGAACA 900

TTGTCTGCGT CTTGAACCGT GAAGTAGAGA GGGTAGCAGT GACTGCAGAG 950

35 GCTTGTAGCC GGCAGCACCG GCTAGACCAG GACAAGATTG AGGCCCTGAG 1000

40 TAACAAGGTG CAACAGCTGG AGAGGAGCAT CGGCCTCAAG GACCTGGCCA 1050

TGGCTGACCT GGAGCAGAAG GTCTCCGAGT TGGAAGTATC CACCTATGAT 1100

GGGGTCTTCA TCTGGAAGAT CTCTGACTTC ACCAGAAAGC GTCAGGAAGC 1150

5 CGTAGCTGGC CGGACACCAG CTATCTTCTC CCCAGCCTTC TACACAAGCA 1200

GATATGGCTA CAAGATGTGT CTACGAGTCT ACTTGAATGG CGACGGCACT 1250

10 GGGCGGGGAA CTCATCTGTC TCTCTTCTTC GTGGTGATGA AAGGCCCCAA 1300

TGATGCTCTG TTGCAGTGGC CTTTAAATCA GAAGGTAACA TTGATGTTGC 1350

15 TGGACCATAA CAACCGGGAG CATGTGATCG ACGCATTGAG GCCCGATGTA 1400

20 ACCTCGTCCT CTTCCAGAG GCCTGTCAGT GACATGAACA TCGCCAGTGG 1450

CTGCCCCCTC TTCTGCCCTG TGTCCAAGAT GGAGGCCAAG AATTCCTATG 1500

25 TGCGGGATGA TGCGATCTTC ATCAAAGCTA TTGTGGACCT AACAGGACTC 1550

TAGCCACCCC TGCTAAGAAT AGCAGCTCAG TGAGGAGCTG TCACATTAGG 1600

30 CCAGCCAGGC CCTGCCACAC ACGGGTGGGC AGGCTTGGTG TAAATGCTGG 1650

35 GGAGGGCCTC AGCCTAGAGC CAATCACCAT CACACAGAAA GGCAGGAAGA
1700

AGCCTCCAGT TGGCCTTCAG CTGGCAAACCT GAGTTGGACG GTCCACTGAG 1750

40 CTCAAGGGCC TGGTGGAGCC CGCTGGGGAG CTTCTCAGCT TTCCAATAGG 1800

AAAGCTCCTG CTGTCTCCTC TGTCTGGGGA AGGGAGAGAC CTGTAGGTGG 1850

GTGCTCAGAA AGGGCCTCTC CAGAGAGAGT CTCAAGAGCT GCAGCAGGAG 1900

CAAAGTGACT GGCCTTCCCC ACCCCATCCT TTGGAAAAGA GGTAGCGGCT 1950

ACACAGGAGA AGGCATGCGC CTGCAGGGTG TAGCCCAAGA GAGAAGCTCT 2000

CTGAGACATA GGCCCTCACT GGAGAAGGGC CTGCCTGGGC TGCACAGCCT 2050

TGCCAGGTGG CCTGTATGGG GGAGAAGTGA TTAAATGTTG AGATGTCACA 2100

CGACAAAAAA AAAAAAAAAA A 2121

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Ala Ala Ser Val Thr Ser Pro Gly Ser Leu Glu Leu Leu
1 5 10 15

Gln Pro Gly Phe Ser Lys Thr Leu Leu Gly Thr Arg Leu Glu Ala
20 25 30

Lys Tyr Leu Cys Ser Ala Cys Lys Asn Ile Leu Arg Arg Pro Phe
35 40 45

Gln Ala Gln Cys Gly His Arg Tyr Cys Ser Phe Cys Leu Thr Ser
50 55 60

Ile Leu Ser Ser Gly Pro Gln Asn Cys Ala Ala Cys Val Tyr Glu

	65	70	75
	Gly Leu Tyr Glu Glu Gly Ile Ser Ile Leu Glu Ser Ser Ser Ala		
	80	85	90
5	Phe Pro Asp Asn Ala Ala Arg Arg Glu Val Glu Ser Leu Pro Ala		
	95	100	105
10	Val Cys Pro Asn Asp Gly Cys Thr Trp Lys Gly Thr Leu Lys Glu		
	110	115	120
	Tyr Glu Ser Cys His Glu Gly Leu Cys Pro Phe Leu Leu Thr Glu		
	125	130	135
15	Cys Pro Ala Cys Lys Gly Leu Val Arg Leu Ser Glu Lys Glu His		
	140	145	150
	His Thr Glu Gln Glu Cys Pro Lys Arg Ser Leu Ser Cys Gln His		
20	155	160	165
	Cys Arg Ala Pro Cys Ser His Val Asp Leu Glu Val His Tyr Glu		
	170	175	180
25	Val Cys Pro Lys Phe Pro Leu Thr Cys Asp Gly Cys Gly Lys Lys		
	185	190	195
	Lys Ile Pro Arg Glu Thr Phe Gln Asp His Val Arg Ala Cys Ser		
	200	205	210
30	Lys Cys Arg Val Leu Cys Arg Phe His Thr Val Gly Cys Ser Glu		
	215	220	225
	Met Val Glu Thr Glu Asn Leu Gln Asp His Glu Leu Gln Arg Leu		
35	230	235	240
	Arg Glu His Leu Ala Leu Leu Leu Ser Ser Phe Leu Glu Ala Gln		
	245	250	255
40	Ala Ser Pro Gly Thr Leu Asn Gln Val Gly Pro Glu Leu Leu Gln		
	260	265	270
	Arg Cys Gln Ile Leu Glu Gln Lys Ile Ala Thr Phe Glu Asn Ile		
	275	280	285

Val Cys Val Leu Asn Arg Glu Val Glu Arg Val Ala Val Thr Ala
290 295 300

5 Glu Ala Cys Ser Arg Gln His Arg Leu Asp Gln Asp Lys Ile Glu
305 310 315

Ala Leu Ser Asn Lys Val Gln Gln Leu Glu Arg Ser Ile Gly Leu
320 325 330

10 Lys Asp Leu Ala Met Ala Asp Leu Glu Gln Lys Val Ser Glu Leu
335 340 345

Glu Val Ser Thr Tyr Asp Gly Val Phe Ile Trp Lys Ile Ser Asp
350 355 360

15 Phe Thr Arg Lys Arg Gln Glu Ala Val Ala Gly Arg Thr Pro Ala
365 370 375

20 Ile Phe Ser Pro Ala Phe Tyr Thr Ser Arg Tyr Gly Tyr Lys Met
380 385 390

Cys Leu Arg Val Tyr Leu Asn Gly Asp Gly Thr Gly Arg Gly Thr
395 400 405

25 His Leu Ser Leu Phe Phe Val Val Met Lys Gly Pro Asn Asp Ala
410 415 420

Leu Leu Gln Trp Pro Phe Asn Gln Lys Val Thr Leu Met Leu Leu
425 430 435

30 Asp His Asn Asn Arg Glu His Val Ile Asp Ala Phe Arg Pro Asp
440 445 450

35 Val Thr Ser Ser Ser Phe Gln Arg Pro Val Ser Asp Met Asn Ile
455 460 465

Ala Ser Gly Cys Pro Leu Phe Cys Pro Val Ser Lys Met Glu Ala
470 475 480

40 Lys Asn Ser Tyr Val Arg Asp Asp Ala Ile Phe Ile Lys Ala Ile
485 490 495

Val Asp Leu Thr Gly Leu
500 501

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Leu Cys Pro Ile Cys Met Gln Ile Ile Lys Asp Ala Phe
 1 5 10 15

Leu Thr Ala Cys Gly His Ser Phe Cys Tyr Met Cys Ile Ile Thr
 20 25 30

His Leu Arg Asn Lys Ser Asp Cys Pro Cys Cys Ser Gln His
 35 40 44

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Leu Ser Cys Ser Ile Cys Leu Glu Pro Phe Lys Glu Pro Val
 1 5 10 15

Thr Thr Pro Cys Gly His Asn Phe Cys Gly Ser Cys Leu Asn Glu
 20 25 30

Thr Trp Ala Val Gln Gly Ser Pro Tyr Leu Cys Pro Gln Cys Arg
 35 40 45

Ala Val
 47

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

141

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5 Leu Leu Arg Cys His Ile Cys Lys Asp Phe Leu Lys Val Pro Val
 1 5 10 15
 Leu Thr Pro Cys Gly His Thr Phe Cys Ser Leu Cys Ile Arg Thr
 20 25 30
 10 His Leu Asn Asn Gln Pro Asn Cys Pro Leu Cys Leu Phe Glu
 35 40 44

(2) INFORMATION FOR SEQ ID NO:8:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

20 Ala Phe Arg Cys His Val Cys Lys Asp Phe Tyr Asp Ser Pro Met
 1 5 10 15
 25 Leu Thr Ser Cys Asn His Thr Phe Cys Ser Leu Cys Ile Arg Arg
 20 25 30
 30 Cys Leu Ser Val Asp Ser Lys Cys Pro Leu Cys Arg Ala Thr
 35 40 44

(2) INFORMATION FOR SEQ ID NO:9:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

40 Ser Ile Ser Cys Gln Ile Cys Glu His Ile Leu Ala Asp Pro Val
 1 5 10 15
 Glu Thr Asn Cys Lys His Val Phe Cys Arg Val Cys Ile Leu Arg

20 25 30
 Cys Leu Lys Val Met Gly Ser Tyr Cys Pro Ser Cys Arg Tyr Pro
 35 40 45

5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Glu Val Thr Cys Pro Ile Cys Leu Asp Pro Phe Val Glu Pro Val
 1 5 10 15

Ser Ile Glu Cys Gly His Ser Phe Cys Gln Glu Cys Ile Ser Gln
 20 25 30

Val Gly Lys Gly Gly Gly Ser Val Cys Ala Val Cys Arg Gln Arg
 35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Glu Leu Met Cys Pro Ile Cys Leu Asp Met Leu Lys Asn Thr Met
 1 5 10 15

Thr Thr Lys Glu Cys Leu His Arg Phe Cys Ser Asp Cys Ile Val
 20 25 30

Thr Ala Leu Arg Ser Gly Asn Lys Glu Cys Pro Thr Cys Arg Lys
 35 40 45

Lys

46

(2) INFORMATION FOR SEQ ID NO:12:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Val Thr Cys Pro Ile Cys Leu Glu Leu Leu Lys Glu Pro Val
1 5 10 15

15 Ser Ala Asp Cys Asn His Ser Phe Cys Arg Ala Cys Ile Thr Leu
20 25 30

Asn Tyr Glu Ser Asn Arg Asn Thr Asp Gly Lys Gly Asn Cys Pro
35 40 45

20 Val Cys Arg Val Pro
50

25 (2) INFORMATION FOR SEQ ID NO:13:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

35 Glu Thr Thr Cys Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met
1 5 10 15

Met Leu Asp Cys Gly His Asn Ile Cys Cys Ala Cys Leu Ala Arg
20 25 30

40 Cys Trp Gly Thr Ala Glu Thr Asn Val Ser Cys Pro Gln Cys Arg
35 40 45

Glu Thr
47

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe Gln Leu Cys Lys Ile Cys Ala Glu Asn Asp Lys Asp Val Lys
 1 5 10 15

Ile Glu Pro Cys Gly His Leu Met Cys Thr Ser Cys Leu Thr Ser
 20 25 30

Trp Gln Glu Ser Glu Gly Gln Gly Ser Ser Gly Cys Pro Phe Cys
 35 40 45

Arg Cys Glu
 48

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Gly Phe Lys Leu Val Thr Cys Asp Phe Cys Lys Arg Asp Asp
 1 5 10 15

Ile Lys Lys Lys Glu Leu Glu Thr His Tyr Lys Thr Cys
 20 25 28

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

145

Gln Asp Leu Ala Val Cys Asp Val Cys Asn Arg Lys Phe Arg His
 1 5 10 15

Lys Asp Tyr Leu Arg Asp His Gln Lys Thr His
 20 25 26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Gly Lys Tyr Pro Phe Ile Cys Ser Glu Cys Gly Lys Ser Phe
 1 5 10 15

Met Asp Lys Arg Tyr Leu Lys Ile His Ser Asn Val His
 20 25 28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Gly Glu Lys Pro Tyr Thr Cys Thr Val Cys Gly Lys Lys Phe
 1 5 10 15

Ile Asp Arg Ser Ser Val Val Lys His Ser Arg Thr His
 20 25 28

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg Lys Lys Phe Pro His Ile Cys Gly Glu Cys Gly Lys Gly Phe
1 5 10 15

Arg His Pro Ser Ala Leu Lys Lys His Ile Arg Val His
20 25 28

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Glu Glu Lys Pro Phe Glu Cys Glu Glu Cys Gly Lys Lys Phe
1 5 10 15

Arg Thr Ala Arg His Leu Val Lys His Gln Arg Ile His
20 25 28

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Pro Asn Glu Gln Met Ala Gln Cys Pro Ile Cys Gln Gln Phe Tyr
1 5 10 15

Pro Leu Lys Ala Leu Glu Lys Thr His Leu Asp Glu Cys
20 25 28

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

1747

Pro Asp Asp Gly Leu Val Ala Cys Pro Ile Cys Leu Thr Arg Met
1 5 10 15

Lys Glu Gln Gln Val Asp Arg His Leu Asp Thr Ser Cys
20 25 28

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCTTGTGCCT GCAGAGAGAA G 21

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAGGTTAAC TTTCGGTGCT CCCCAGCAGG GTCTC 35

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTAGGTTAAC TGGAGAAGGG GACCTGCTCG TCCTT 35

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTAGGTTAAC TGCTGGCTTG GGAGGAGCAC TGTGA 35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTAGGTTAAC TGCTCCCGGT GCTGGCCCGG GCCTC 35

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGGTTAAC TGC ACTGGCC GAGCTCTCCA GGGA 34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGATGAGAA TTCAT 15

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGATGAATTC TCATCACTGC A 21

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GATCGGATCC AAAAAGAAGC CCTTGTGCCT GCA 33

5

(2) INFORMATION FOR SEQ ID NO:32:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCCTGGTTAA CTGGGC 16

20

(2) INFORMATION FOR SEQ ID NO:33:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCNCCNATGG CNYTNGARC 19

35

(2) INFORMATION FOR SEQ ID NO:34:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCNCCNATGG CNYTNGARA 19

5

(2) INFORMATION FOR SEQ ID NO:35:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCNCCNATGG CNYTNGARG 19

20

(2) INFORMATION FOR SEQ ID NO:36:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GYTCNARNGC CATNGGNGC 19

35

(2) INFORMATION FOR SEQ ID NO:37:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TYTCNARNGC CATNGGNGC 19

5

(2) INFORMATION FOR SEQ ID NO:38:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CYTCNARNGC CATNGGNGC 19

20

(2) INFORMATION FOR SEQ ID NO:39:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AARCAYGCNT AYG TNAA 17

35

(2) INFORMATION FOR SEQ ID NO:40:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTNACRTANG CRTGYTT 17

5

(2) INFORMATION FOR SEQ ID NO:41:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ala Pro Met Ala Leu Glu Arg
1 5 7

20 (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

30 Lys His Ala Tyr Val Lys
1 5 6

(2) INFORMATION FOR SEQ ID NO:43:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

40

Pro Gly Ser Asn Leu Gly Ser
1 5 7

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Lys Asp Asp Thr Met Phe Leu Lys

1 5 8

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCGATCGTCG ACCAAAAAGA AGCCCTCCTG CCTACAA 37

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTAGAGATCT CAGGGGTCAG GCCACTTT 28

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 bases

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTAGAGATCT GTTAACTTTC GGTGCTCCCC AGCAGGGTCT C 41

10

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 41 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTAGAGATCT GTTAACTGGA GAAGGGGACC TGCTCGTCCT T 41

25

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 41 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTAGAGATCT GTTAACTGCT GGCTTGGGAG GAGCACTGTG A 41

40

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

PA01972g.cip

- (A) LENGTH: 37 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCGATCGTCG ACCAAAAAGA AGCCCTCCTG CCTACAA 37

10

(2) INFORMATION FOR SEQ ID NO:51:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTAGAGATCT CAGGGGTCAG GCCACTTT 28

25

(2) INFORMATION FOR SEQ ID NO:52:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TCGATCGTCG ACCGCCTCCA GCTCAGCCCC TGAT 34

40

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GATCGGATCC GGAGACACAG ATTCCAGCCC C 31

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GATCGAATTC TTA ACTCTTC GGTGCTCCCC AGCAG 35

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CCTGGCTGGC CTAATGT 17

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GATCGACTCG AGATGCCCAA GAAGAAGCGG AAGGTGGCTG CAGCCAGTGT 50

GACTTCCCCT 60

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTCTGGCGAA GAAGTCC 17

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GATCGGATCC GCCTCCAGCT CAGCCCCTGA T 31

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GATCGGATCC AGCCAGCAGC TTCTCCTTCA C 31

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30

160

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GATCGGATCC GCTCAGGCTC TTTTGGGGCA 30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GATCGAGTCG ACCAGTAGTT CGGCCTTTCA AGAT 34

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CTCTGGCGAA GAAGTCC 17

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GATCGAGTCG ACCGTGGGGC CAGAGCTACT CCAG 34

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTACGTGCGG CCGCCTACCA CCTGGTTCAA GGTCCTG 38